

SEQUENCE LISTING

5 <110> Lassner, M
Post-Beittenmiller, D
Savidge, B
Weiss, J

10 <120> Nucleic Acid Sequences Involved in
Tocopherol Synthesis

<130> 17133/02/US

5 <150> 60/129,899
<151> 1999-04-15

<150> 60/146,461
<151> 1999-07-30

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Arg Asn Asn Leu Val Arg Pro Asp Gly Gln Gly Ser Ser Leu Leu Leu
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Tyr Pro Lys His Lys Ser Arg Phe Arg Val Asn Ala Thr Ala Gly Gln
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Pro Glu Ala Phe Asp Ser Asn Ser Lys Gln Lys Ser Phe Arg Asp Ser
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Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr
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Asp Ile Ser Pro Leu Leu Phe Thr Gly Ile Leu Glu Ala Val Val Ala
130 135 140
35 Ala Leu Met Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu Ser Asp
145 150 155 160
Val Glu Ile Asp Lys Val Asn Lys Pro Tyr Leu Pro Leu Ala Ser Gly
165 170 175
Glu Tyr Ser Val Asn Thr Gly Ile Ala Ile Val Ala Ser Phe Ser Ile
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40 Met Ser Phe Trp Leu Gly Trp Ile Val Gly Ser Trp Pro Leu Phe Trp

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5 225 230 235 240
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Pro Phe Ile Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu
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35 40 45
Thr Lys Cys Tyr Pro Ser Trp Asn Asp Asn Tyr Gln Val Trp Ser Lys
50 55 60
Gly Arg Glu Leu His Gln Glu Lys Phe Phe Gly Val Gly Trp Asn Tyr
65 70 75 80
30 Arg Leu Ile Cys Gly Met Ser Ser Ser Ser Ser Val Leu Glu Gly Lys
85 90 95
Pro Lys Lys Asp Asp Lys Glu Lys Ser Asp Gly Val Val Val Lys Lys
100 105 110
Ala Ser Trp Ile Asp Leu Tyr Leu Pro Glu Glu Val Arg Gly Tyr Ala
115 120 125
35 Lys Leu Ala Arg Leu Asp Lys Pro Ile Gly Thr Trp Leu Leu Ala Trp
130 135 140
Pro Cys Met Trp Ser Ile Ala Leu Ala Ala Asp Pro Gly Ser Leu Pro
145 150 155 160
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165 170 175

Gly Ala Gly Cys Thr Ile Asn Asp Leu Leu Asp Gln Asp Ile Asp Thr
180 185 190
Lys Val Asp Arg Thr Lys Leu Arg Pro Ile Ala Ser Gly Leu Leu Thr
195 200 205
5 Pro Phe Gln Gly Ile Gly Phe Leu Gly Leu Gln Leu Leu Leu Gly Leu
210 215 220
Gly Ile Leu Leu Gln Leu Asn Asn Tyr Ser Arg Val Leu Gly Ala Ser
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Trp Pro Gln Ala Phe Leu Gly Leu Thr Ile Asn Trp Gly Ala Leu Leu
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Gly Trp Thr Ala Val Lys Gly Ser Ile Ala Pro Ser Ile Val Leu Pro
275 280 285
5 Leu Tyr Leu Ser Gly Val Cys Trp Thr Leu Val Tyr Asp Thr Ile Tyr
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Ala Leu Arg Phe Gly Asp Asn Thr Lys Leu Trp Leu Thr Gly Phe Gly
325 330 335
10 Thr Ala Ser Ile Gly Phe Leu Ala Leu Ser Gly Phe Ser Ala Asp Leu
340 345 350
Gly Trp Gln Tyr Tyr Ala Ser Leu Ala Ala Ala Ser Gly Gln Leu Gly
355 360 365
5 Trp Gln Ile Gly Thr Ala Asp Leu Ser Ser Gly Ala Asp Cys Ser Arg
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35 40 45
Ala Lys Leu Gly Ile Thr Gly Val Arg Ser Asp Ala Asn Arg Val Phe
50 55 60
Ala Thr Ala Thr Ala Ala Ala Thr Ala Thr Ala Thr Thr Gly Glu Ile
35 65 70 75 80
Ser Ser Arg Val Ala Ala Leu Ala Gly Leu Gly His His Tyr Ala Arg
85 90 95
Cys Tyr Trp Glu Leu Ser Lys Ala Lys Leu Ser Met Leu Val Val Ala
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40 Thr Ser Gly Thr Gly Tyr Ile Leu Gly Thr Gly Asn Ala Ala Ile Ser
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Phe Pro Gly Leu Cys Tyr Thr Cys Ala Gly Thr Met Met Ile Ala Ala
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 5 Met Lys Arg Thr Met Leu Arg Pro Leu Pro Ser Gly Arg Ile Ser Val
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 10 195 200 205
 Asn Leu Val Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Gln Leu His
 210 215 220
 Pro Ile Asn Thr Trp Val Gly Ala Val Val Gly Ala Ile Pro Pro Leu
 225 230 235 240
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 Leu Pro Ala Ala Leu Tyr Phe Trp Gln Ile Pro His Phe Met Ala Leu
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 Ala His Leu Cys Arg Asn Asp Tyr Ala Ala Gly Gly Tyr Lys Met Leu
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 25 Leu Thr Ser Ser Trp Phe Cys Leu Glu Ser Thr Leu Leu Thr Leu Ala
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 Ile Ala Ala Thr Ala Phe Ser Phe Tyr Arg Asp Arg Thr Met His Lys
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 Ala Arg Lys Met Phe His Ala Ser Leu Leu Phe Leu Pro Val Phe Met
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 Val Glu Glu Ala Gly Leu Thr Asn Ser Val Ser Gly Glu Val Lys Thr
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	tccgtgaaat acctgcgggc gtcatactctg ccaacagtgc gctgggtgtt acgataggct	420
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35 40 45
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50 55 60
Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
10 65 70 75 80
Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn
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Val Val Met Gly Asn Lys Val Val Ala Leu Leu Ala Thr Ala Val Glu
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15 His Leu Val Thr Gly Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln
115 120 125
Arg Tyr Ser Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala
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Ser Leu Ile Ser Asn Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln
145 150 155 160
20 Thr Ala Glu Val Ala Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly
165 170 175
Leu Ala Phe Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser
180 185 190
25 Ala Ser Leu Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile
195 200 205
Thr Ala Pro Ile Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu
210 215 220
Val Val Asp Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu
225 230 235 240
30 Glu Tyr Leu Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala
245 250 255
Met Glu His Ala Asn Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu
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35 40 45
10 Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg Gln Arg Gly
50 55 60
Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
65 70 75 80
5 Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn
85 90 95
Val Val Met Gly Asn Lys Met Ser Val Leu Ala Gly Asp Phe Leu Leu
100 105 110
Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr Glu Val Val
115 120 125
20 Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly Glu Thr Met
130 135 140
Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp Tyr Tyr Met
145 150 155 160
5 Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn Ser Cys Lys
165 170 175
Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu Val Ala Val Leu Ala
180 185 190
Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu Ile Asp Asp
195 200 205
30 Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys Gly Ser Leu
210 215 220
Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu Phe Ala Met
225 230 235 240
35 Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val Glu Lys Asp
245 250 255
Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys Ser Lys Gly
260 265 270
Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn Leu Ala Ala
275 280 285
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gtttaaactc tgtgtataat tgcaggaaag gaaacagttc atgagctttt cggcacaaga 120
gtagcgggtgc tagctggaga tttcatgttt gctcaagcgt catggtactt agcaaatctc 180
gagaatcttg aagttattaa gctcatcagt cagggtactta gttactctta cattgttttt 240
ctatgagggtt gagctatgaa tctcatttcg ttgaataatg ctgtgcctca aacttttttt 300
catgttttca ggtgatcaaa gactttgcaa gcggagagat aaagcaggcg tccagcttat 360
ttgactgcga caccaagctc gacgagtact tactcaaaag tttctacaag acagcctctt 420
tagtggtgc gagcaccaaa ggagctgcc ttttcagcag agttgagcct gatgtgacag 480
aacaatgta cgagtttggg aagaatctcg gtctctcttt ccagatagtt gatgatattt 540
40 tggatttcac tcagtcgaca gagcagctcg ggaagccagc agggagtgat ttggctaaag 600
gtaacttaac agcacctgtg attttcgctc tggagaggga gccaaaggcta agagagatca 660

ttgagtcaaa gttctgtgag gcgggttctc tggaagaagc gattgaagcg gtgacaaaag 720
gtgggggggat taagagagca c 741

<210> 15

5 <211> 1087

<212> DNA

<213> Arabidopsis sp

<400> 15

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ttcaaccaga gggaaaaagc aacgataaca actctgcttt tgatttcaag ctgtatatga 180
tccgcaaagc cgagtctgta aatgcggctc tcgacgtttc cgtaccgctt ctgaaacccc 240
ttacgatcca agaagcggtc aggtactctt tgctagccgg cggaaaaagc gtgaggcctc 300
5 tgctctgcat tgccgcttgt gagcttgtgg ggggcgacga ggctactgcc atgtcagccg 360
cttgcgcggt cgagatgac cacacaagct ctctcattca tgacgatctt ccgtgcatgg 420
acaatgccga cctccgtaga ggcaagccca ccaatcacaa ggtatgttgt ttaattatat 480
gaaggctcag agataatgct gaactagtgt tgaaccaatt tttgctcaa caaggtatat 540
ggagaagaca tggcggtttt ggcaggtgat gcactccttg cattggcggt tgagcacatg 600
20 acggttgtgt cgagtgggtt ggtcgctccc gagaagatga ttcgcgccgt ggttgagctg 660
gccagggcca tagggactac agggctagtt gctggacaaa tgatagacct agccagcgaa 720
agactgaatc cagacaaggt tggattggag catctagagt tcatccatct ccacaaaacg 780
gcggcattgt tggaggcagc ggcagtttta ggggttataa tgggaggtgg aacagaggaa 840
gaaatcgaag agcttagaaa gtatgctagg tgtattggac tactgtttca ggttgttgat 900
5 gacattctcg acgtaacaaa atctactgag gaattgggta agacagccgg aaaagacgta 960
atggccggaa agctgacgta tccaaggctg ataggtttg agggatccag ggaagttgca 1020
gagcacctga ggagagaagc agaggaaaag cttaaagggt ttgatccaag tcaggcggcg 1080
cctctgg 1087

30 <210> 16

<211> 1164

<212> DNA

<213> Arabidopsis sp

35 <400> 16

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ggtttctcga cgttgatcta cgaatcaccg gggcgagat ttgttggtcg tgcggcgag 180
actgatactg ataaagttaa atctcagaca cctgacaagg caccagccgg tggttcaagc 240
40 attaaccagc ttctcggtat caaaggagca tctcaagaaa ctaataaatg gaagattcgt 300
cttcagctta caaaaccagt cacttggcct ccactgggtt ggggagtcgt ctgtggtgct 360

gctgcttcag ggaactttca ttggacccca gaggatgttg ctaagtcgat tctttgcatg 420
atgatgtctg gtccttgtct tactggctat acacagacaa tcaacgactg gtatgataga 480
gatatcgacg caattaatga gccatatcgt ccaattccat ctggagcaat atcagagcca 540
gaggttatta cacaagtctg ggtgctatta ttgggaggtc ttggtattgc tggaaatatta 600
5 gatgtgtggg cagggcatac cactcccact gtcttctatc ttgctttggg aggatcattg 660
ctatcttata tatactctgc tccacctctt aagctaaaac aaaatggatg ggttggaat 720
tttgacttg gagcaagcta tattagtgtt ccattggtgg ctggccaagc attgtttggc 780
actcttacgc cagatgttgt tgttctaaca ctcttgtaga gcatagctgg gtttaggaata 840
gccattgtta acgacttcaa aagtgttgaa ggagatagag cattaggact tcagtctctc 900
10 ccagtagctt ttggcaccga aactgcaaaa tggatatgcy ttggtgctat agacattact 960
cagctttctg ttgccggata tctattagca tctgggaaac cttattatgc gttggcggtg 1020
gttgctttga tcattcctca gattgtgttc cagtttaaat actttctcaa ggaccctgtc 1080
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<210> 17

<211> 387

<212> PRT

<213> Arabidopsis sp

<400> 17

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Thr Ser Val Asp Arg Val Gly Val Leu Ser Leu Arg Asn Ser Asp Ser
20 25 30
Val Glu Phe Thr Arg Arg Arg Ser Gly Phe Ser Thr Leu Ile Tyr Glu
35 40 45
Ser Pro Gly Arg Arg Phe Val Val Arg Ala Ala Glu Thr Asp Thr Asp
50 55 60
30 Lys Val Lys Ser Gln Thr Pro Asp Lys Ala Pro Ala Gly Gly Ser Ser
65 70 75 80
Ile Asn Gln Leu Leu Gly Ile Lys Gly Ala Ser Gln Glu Thr Asn Lys
85 90 95
Trp Lys Ile Arg Leu Gln Leu Thr Lys Pro Val Thr Trp Pro Pro Leu
100 105 110
35 Val Trp Gly Val Val Cys Gly Ala Ala Ala Ser Gly Asn Phe His Trp
115 120 125
Thr Pro Glu Asp Val Ala Lys Ser Ile Leu Cys Met Met Met Ser Gly
130 135 140
40 Pro Cys Leu Thr Gly Tyr Thr Gln Thr Ile Asn Asp Trp Tyr Asp Arg
145 150 155 160

Asp Ile Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala
165 170 175
Ile Ser Glu Pro Glu Val Ile Thr Gln Val Trp Val Leu Leu Leu Gly
180 185 190
5 Gly Leu Gly Ile Ala Gly Ile Leu Asp Val Trp Ala Gly His Thr Thr
195 200 205
Pro Thr Val Phe Tyr Leu Ala Leu Gly Gly Ser Leu Leu Ser Tyr Ile
210 215 220
Tyr Ser Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Val Gly Asn
10 225 230 235 240
Phe Ala Leu Gly Ala Ser Tyr Ile Ser Leu Pro Trp Trp Ala Gly Gln
245 250 255
Ala Leu Phe Gly Thr Leu Thr Pro Asp Val Val Val Leu Thr Leu Leu
260 265 270
15 Tyr Ser Ile Ala Gly Leu Gly Ile Ala Ile Val Asn Asp Phe Lys Ser
275 280 285
Val Glu Gly Asp Arg Ala Leu Gly Leu Gln Ser Leu Pro Val Ala Phe
290 295 300
Gly Thr Glu Thr Ala Lys Trp Ile Cys Val Gly Ala Ile Asp Ile Thr
20 305 310 315 320
Gln Leu Ser Val Ala Gly Tyr Leu Leu Ala Ser Gly Lys Pro Tyr Tyr
325 330 335
Ala Leu Ala Leu Val Ala Leu Ile Ile Pro Gln Ile Val Phe Gln Phe
340 345 350
15 Lys Tyr Phe Leu Lys Asp Pro Val Lys Tyr Asp Val Lys Tyr Gln Ala
355 360 365
Ser Ala Gln Pro Phe Leu Val Leu Gly Ile Phe Val Thr Ala Leu Ala
370 375 380
Ser Gln His
30 385

<210> 18

<211> 981

<212> DNA

35 <213> Arabidopsis sp

<400> 18

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cacactcttc ctatgaaact ctctcccgt gcaatccgat cttcatcctc atctgccccg 120
40 gggtcgttga acttcgatct gaggacgtat tggacgactc tgatcaccga gatcaaccag 180
aagctggatg aggccatacc ggtcaagcac cctgcgggga tctacgaggc tatgagatac 240

	tctgtactcg cacaaggcgc caagcgtgcc cctcctgtga tgtgtgtggc ggcctgcgag	300
	ctcttcggtg gcgatgcct cgccgcttc cccaccgcct gtgccctaga aatggtgcac	360
	gcggttcgt tgatacacga cgacctccc tgtatggacg acgatcctgt gcgcagagga	420
	aagccatcta accacactgt ctacggctct ggcatggcca ttctcgccgg tgacgcctc	480
5	ttccactcg ccttcagca cattgtctcc cacacgcctc ctgacctgt tccccgagcc	540
	accatcctca gactcatcac tgagattgcc cgcactgtcg gctccactgg tatggctgca	600
	ggccagtacg tcgacctga aggaggtccc ttccctcttt cctttgttca ggagaagaaa	660
	ttcgagacca tgggtgaatg ctctgccgtg tgcggtggcc tattgggagg tgccactgag	720
	gatgagctcc agagtctccg aaggtacggg agagccgtcg ggatgctgta tcaggtggtc	780
10	gatgacatca ccgaggacaa gaagaagagc tatgatggtg gagcagagaa gggaatgatg	840
	gaaatggcgg aagagctcaa ggagaaggcg aagaaggagc ttcaagtgtt tgacaacaag	900
	tatggaggag gagacacact tgttcctctc tacaccttcg ttgactacgc tgctcatcga	960
	cattttcttc ttcccctctg a	981

15 <210> 19
<211> 245
<212> DNA
<213> GLycine sp

20 <400> 19
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tcttgactt gcttgggtac catgatggtt gctgcatctg ctaactcttt gaatcaggtg 120
tttgagatca ataatgatgc taaaatgaag agaacaagtc gcaggccact accctcagga 180
cgcatcacia tacctcatgc agttggctgg gcatcctctg ttggattagc tggtagggct 240
ctact 245

25 <210> 20
<211> 253
<212> DNA
30 <213> Glycine sp

<400> 20
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ttggcattgt ccaaggatat acctgacgtt gaaggagata aagagcacgg cattgattct 120
35 tttgcagtac gtctaggtca gaaacgggca ttttgattt gcgtttcctt ttttgaaatg 180
gctttcggag ttggtatcct ggccggagca tcatgctcac acttttggac taaaattttc 240
acgggtatgg gaa 253

40 <210> 21
<211> 275
<212> DNA

<213> Glycine sp

<400> 21

	tgatcttcta ctctctgggt atggcattgt ccaaggatat atctgacgtt aaaggagata	60
5	aagcatacgg catcgatact ttagcgatac gtttgggtca aaaatgggta ttttggattt	120
	gcattatcct ttttgaaatg gcttttggag ttgccctctt ggcaggagca acatcttctt	180
	acctttggat taaaattgtc acgggtctgg gacatgctat tcttgcttca attctcttgt	240
	accaagccaa atctatatac ttgagcaaca aagtt	275

10 <210> 22

<211> 299

<212> DNA

<213> Glycine sp

15 <220>

<221> misc_feature

<222> (1)...(299)

<223> n = A,T,C or G

20 <400> 22

	ccanaatang tncatcttng aaagacaatt ggccctcttca acacacaagt ctgcatgtga	60
	agaagaggcc aattgtcttt ccaagatcac ttatngtggc tattgtaatc atgaacttct	120
	tctttgtggg tatggcattg gcaaaggata tacctanctg ttgaaggaga taaaatatat	180
	ggcattgata cttttgcaat acgtataggt caaaaacaag tattttggat ttgtattttc	240
25	ctttttgaaa ggctttcgga gtttccctag tggcaggagc aacatcttct agccttggt	299

<210> 23

<211> 767

<212> DNA

30 <213> Glycine sp

<400> 23

	gtggaggctg tggttgctgc cctgtttatg aatatttata ttgttggttt gaatcaattg	60
	tctgatgttg aaatagacaa gataaacaag ccgtatcttc cattagcatc tggggaatat	120
35	tcctttgaaa ctggtgtcac tattgttgca tctttttcaa ttctgagttt ttggcttggc	180
	tgggtttagt gttcatggcc attatttttg gccctttttg taagctttgt gctaggaact	240
	gcttattcaa tcaatgtgcc tctgttgaga tggaaagagg ttgcagtgtc tgcagcgatg	300
	tgcattctag ctgttcgggc agtaatagtt caacttgcac ttttccttca catgcagact	360
	catgtgtaca agaggccacc tgtcttttca agaccattga tttttgctac tgcattcatg	420
40	agcttcttct ctgtagtatt agcactgttt aaggatatac ctgacattga aggagataaa	480
	gtattttggca tccaatcttt ttcagtgtgt ttaggtcaga agccggtgtt ctggacttgt	540

gttacccttc ttgaaatagc ttatggagtc gccctcctgg tgggagctgc atctccttgt 600
ctttggagca aaattttcac gggctctggga cacgctgtgc tggcttcaat tctctggttt 660
catgccaaat ctgtagattt gaaaagcaaa gcttcgataa catccttcta tatgtttatt 720
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5

<210> 24
<211> 255
<212> PRT
<213> Glycine sp

10

<400> 24
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Leu Asn Gln Leu Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr
20 25 30
Leu Pro Leu Ala Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile
35 40 45
Val Ala Ser Phe Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly
50 55 60
Ser Trp Pro Leu Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr
65 70 75 80
Ala Tyr Ser Ile Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val
85 90 95
Leu Ala Ala Met Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu
100 105 110
Ala Phe Phe Leu His Met Gln Thr His Val Tyr Lys Arg Pro Pro Val
115 120 125
Phe Ser Arg Pro Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser
130 135 140
30 Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys
145 150 155 160
Val Phe Gly Ile Gln Ser Phe Ser Val Cys Leu Gly Gln Lys Pro Val
165 170 175
Phe Trp Thr Cys Val Thr Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu
180 185 190
35 Leu Val Gly Ala Ala Ser Pro Cys Leu Trp Ser Lys Ile Phe Thr Gly
195 200 205
Leu Gly His Ala Val Leu Ala Ser Ile Leu Trp Phe His Ala Lys Ser
210 215 220
40 Val Asp Leu Lys Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met Phe Ile
225 230 235 240

Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val Arg
245 250 255

<210> 25

5 <211> 360

<212> DNA

<213> Zea sp

<220>

10 <221> misc_feature

<222> (1)...(360)

<223> n = A,T,C or G

<400> 25

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tcaggcttat cttggcctga cattcaactg gggagcttta ctagggtggg ctgctattaa 120
ggaaagcata gaccctgcaa atcatccttc cattgtatac agctgggtatt tgttggacgc 180
tggtgtatga tactatatat gcgcacacagg tgtttcgcta tccctacttt catattaatc 240
cttgatgaag tggccatttc atgtttgtcgc ggtgggtctta tacttgcata tctccatgca 300
0 tctcaggaca aagangatga cctgaaagta ggagtccaag tccacagctt aagatttggg 360

<210> 26

<211> 299

<212> DNA

5 <213> Zea sp

<220>

<221> misc_feature

<222> (1)...(299)

30 <223> n = A,T,C or G

<400> 26

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aatgaaaagg acaatgcgtg cccctgcca tctggctgca ttagtcctgc acatgctgcg 120
35 atgtgggcta caagtgttgg agttgcagga acagctttgt tggcctggaa ggctaattggc 180
ttggcagctg ggcttgcagc ttctaattctt gttctgtatg catttgtgta tacgccgttg 240
aagcaaatac accctgttaa tacatgggtt ggggcagtcg ttggtgccat cccaccact 299

<210> 27

40 <211> 255

<212> DNA

<213> Zea sp

<220>

<221> misc_feature

5 <222> (1)...(255)

<223> n = A,T,C or G

<400> 27

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10	tccacagcat taagatttgg agatttgacc nnatactgna tcagtggctt tggcgcgga	120
	tgcttcggca gcttagcact cagtggttac aatgctgacc ttggttggtg tttagtgtga	180
	tgcttgagcg aagaatggta tngtttttac ttgatattga ctccagacct gaaatcatgt	240
	tggaacagggt ggccc	255

<210> 28

<211> 257

<212> DNA

<213> Zea sp

<400> 28

	attgaagggg ataggactct ggggcttcag tcacttcctg ttgcttttgg gatggaaact	60
	gcaaaatgga tttgtgttgg agcaattgat atcactcaat tatctgttgc aggttaccta	120
	ttgagcaccg gtaagctgta ttatgccctg gtgttgcttg ggctaacaat tcctcagggtg	180
	ttctttcagt tccagtactt cctgaaggac cctgtgaagt atgatgtcaa atatcaggga	240
	agcgacacaac cattctt	257

<210> 29

<211> 368

<212> DNA

30 <213> Zea sp

<400> 29

	atccagttgc aaataataat ggcgttcttc tctgttgtaa tagcactatt caaggatata	60
	cctgacatcg aaggggaccg catattcggg atccgatacct tcagcgctcg gttagggcaa	120
35	aagaaggtct tttggatctg cgttggttg cttgagatgg cctacagcgt tgcgatactg	180
	atgggagcta cctcttctg tttgtggagc aaaacagcaa ccatcgctgg ccattccata	240
	cttgccgcga tcctatggag ctgcgcgcga tcggtggact tgacgagcaa agccgcaata	300
	acgtccttct acatgttcat ctggaagctg ttctacgcgg agtacctgct catccctctg	360
	gtgcggtg	368

40

<210> 30

<211> 122
<212> PRT
<213> Zea sp

5 <400> 30
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Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Arg Ile Phe Gly Ile Arg
20 25 30
10 Ser Phe Ser Val Arg Leu Gly Gln Lys Lys Val Phe Trp Ile Cys Val
35 40 45
Gly Leu Leu Glu Met Ala Tyr Ser Val Ala Ile Leu Met Gly Ala Thr
50 55 60
Ser Ser Cys Leu Trp Ser Lys Thr Ala Thr Ile Ala Gly His Ser Ile
65 70 75 80
Leu Ala Ala Ile Leu Trp Ser Cys Ala Arg Ser Val Asp Leu Thr Ser
85 90 95
Lys Ala Ala Ile Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr
100 105 110
20 Ala Glu Tyr Leu Leu Ile Pro Leu Val Arg
115 120

<210> 31
<211> 278
<212> DNA
<213> Zea sp

30 <400> 31
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gcgagttaca tcagcttgcc ctggtgggct ggccaggcgt tatttggaac ttttacacca 120
gatatcattg tcttgactac tttgtacagc atagctgggc tagggattgc tattgtaaat 180
gatttcaaga gtattgaagg ggataggact ctggggcttc agtcacttcc tgttgctttt 240
gggatggaaa ctgcaaaatg gatttgtgtt ggagcaat 278

35 <210> 32
<211> 292
<212> PRT
<213> Synechocystis sp

40 <400> 32
Met Val Ala Gln Thr Pro Ser Ser Pro Pro Leu Trp Leu Thr Ile Ile

1 5 10 15
Tyr Leu Leu Arg Trp His Lys Pro Ala Gly Arg Leu Ile Leu Met Ile
20 25 30
Pro Ala Leu Trp Ala Val Cys Leu Ala Ala Gln Gly Leu Pro Pro Leu
5 35 40 45
Pro Leu Leu Gly Thr Ile Ala Leu Gly Thr Leu Ala Thr Ser Gly Leu
50 55 60
Gly Cys Val Val Asn Asp Leu Trp Asp Arg Asp Ile Asp Pro Gln Val
65 70 75 80
10 Glu Arg Thr Lys Gln Arg Pro Leu Ala Ala Arg Ala Leu Ser Val Gln
85 90 95
Val Gly Ile Gly Val Ala Leu Val Ala Leu Leu Cys Ala Ala Gly Leu
100 105 110
Ala Phe Tyr Leu Thr Pro Leu Ser Phe Trp Leu Cys Val Ala Ala Val
115 120 125
Pro Val Ile Val Ala Tyr Pro Gly Ala Lys Arg Val Phe Pro Val Pro
130 135 140
Gln Leu Val Leu Ser Ile Ala Trp Gly Phe Ala Val Leu Ile Ser Trp
145 150 155 160
20 Ser Ala Val Thr Gly Asp Leu Thr Asp Ala Thr Trp Val Leu Trp Gly
165 170 175
Ala Thr Val Phe Trp Thr Leu Gly Phe Asp Thr Val Tyr Ala Met Ala
180 185 190
Asp Arg Glu Asp Asp Arg Arg Ile Gly Val Asn Ser Ser Ala Leu Phe
195 200 205
25 Phe Gly Gln Tyr Val Gly Glu Ala Val Gly Ile Phe Phe Ala Leu Thr
210 215 220
Ile Gly Cys Leu Phe Tyr Leu Gly Met Ile Leu Met Leu Asn Pro Leu
225 230 235 240
30 Tyr Trp Leu Ser Leu Ala Ile Ala Ile Val Gly Trp Val Ile Gln Tyr
245 250 255
Ile Gln Leu Ser Ala Pro Thr Pro Glu Pro Lys Leu Tyr Gly Gln Ile
260 265 270
Phe Gly Gln Asn Val Ile Ile Gly Phe Val Leu Leu Ala Gly Met Leu
35 275 280 285
Leu Gly Trp Leu
290

<210> 33

40 <211> 316

<212> PRT

<213> Synechocystis sp

<400> 33

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20 25 30
Leu Leu Ile Thr Thr Ala Ala Ser Met Trp Ile Ala Ser Glu Gly Arg
35 40 45
10 Val Asp Leu Pro Lys Leu Leu Ile Thr Leu Leu Gly Gly Thr Leu Ala
50 55 60
Ala Ala Ser Ala Gln Thr Leu Asn Cys Ile Tyr Asp Gln Asp Ile Asp
65 70 75 80
Tyr Glu Met Leu Arg Thr Arg Ala Arg Pro Ile Pro Ala Gly Lys Val
85 90 95
Gln Pro Arg His Ala Leu Ile Phe Ala Leu Ala Leu Gly Val Leu Ser
100 105 110
Phe Ala Leu Leu Ala Thr Phe Val Asn Val Leu Ser Gly Cys Leu Ala
115 120 125
20 Leu Ser Gly Ile Val Phe Tyr Met Leu Val Tyr Thr His Trp Leu Lys
130 135 140
Arg His Thr Ala Gln Asn Ile Val Ile Gly Gly Ala Ala Gly Ser Ile
145 150 155 160
Pro Pro Leu Val Gly Trp Ala Ala Val Thr Gly Asp Leu Ser Trp Thr
165 170 175
25 Pro Trp Val Leu Phe Ala Leu Ile Phe Leu Trp Thr Pro Pro His Phe
180 185 190
Trp Ala Leu Ala Leu Met Ile Lys Asp Asp Tyr Ala Gln Val Asn Val
195 200 205
30 Pro Met Leu Pro Val Ile Ala Gly Glu Glu Lys Thr Val Ser Gln Ile
210 215 220
Trp Tyr Tyr Ser Leu Leu Val Val Pro Phe Ser Leu Leu Leu Val Tyr
225 230 235 240
Pro Leu His Gln Leu Gly Ile Leu Tyr Leu Ala Ile Ala Ile Ile Leu
245 250 255
35 Gly Gly Gln Phe Leu Val Lys Ala Trp Gln Leu Lys Gln Ala Pro Gly
260 265 270
Asp Arg Asp Leu Ala Arg Gly Leu Phe Lys Phe Ser Ile Phe Tyr Leu
275 280 285
40 Met Leu Leu Cys Leu Ala Met Val Ile Asp Ser Leu Pro Val Thr His
290 295 300

Gln Leu Val Ala Gln Met Gly Thr Leu Leu Leu Gly
305 310 315

<210> 34

5 <211> 324

<212> PRT

<213> Synechocystis sp

<400> 34

10 Met Ser Asp Thr Gln Asn Thr Gly Gln Asn Gln Ala Lys Ala Arg Gln
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Leu Leu Gly Met Lys Gly Ala Ala Pro Gly Glu Ser Ser Ile Trp Lys
20 25 30
Ile Arg Leu Gln Leu Met Lys Pro Ile Thr Trp Ile Pro Leu Ile Trp
35 40 45
Gly Val Val Cys Gly Ala Ala Ser Ser Gly Gly Tyr Ile Trp Ser Val
50 55 60
Glu Asp Phe Leu Lys Ala Leu Thr Cys Met Leu Leu Ser Gly Pro Leu
65 70 75 80
20 Met Thr Gly Tyr Thr Gln Thr Leu Asn Asp Phe Tyr Asp Arg Asp Ile
85 90 95
Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala Ile Ser
100 105 110
Val Pro Gln Val Val Thr Gln Ile Leu Ile Leu Leu Val Ala Gly Ile
115 120 125
15 Gly Val Ala Tyr Gly Leu Asp Val Trp Ala Gln His Asp Phe Pro Ile
130 135 140
Met Met Val Leu Thr Leu Gly Gly Ala Phe Val Ala Tyr Ile Tyr Ser
145 150 155 160
30 Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Leu Gly Asn Tyr Ala
165 170 175
Leu Gly Ala Ser Tyr Ile Ala Leu Pro Trp Trp Ala Gly His Ala Leu
180 185 190
Phe Gly Thr Leu Asn Pro Thr Ile Met Val Leu Thr Leu Ile Tyr Ser
195 200 205
35 Leu Ala Gly Leu Gly Ile Ala Val Val Asn Asp Phe Lys Ser Val Glu
210 215 220
Gly Asp Arg Gln Leu Gly Leu Lys Ser Leu Pro Val Met Phe Gly Ile
225 230 235 240
40 Gly Thr Ala Ala Trp Ile Cys Val Ile Met Ile Asp Val Phe Gln Ala
245 250 255

Gly Ile Ala Gly Tyr Leu Ile Tyr Val His Gln Gln Leu Tyr Ala Thr
260 265 270
Ile Val Leu Leu Leu Leu Ile Pro Gln Ile Thr Phe Gln Asp Met Tyr
275 280 285
5 Phe Leu Arg Asn Pro Leu Glu Asn Asp Val Lys Tyr Gln Ala Ser Ala
290 295 300
Gln Pro Phe Leu Val Phe Gly Met Leu Ala Thr Gly Leu Ala Leu Gly
305 310 315 320
His Ala Gly Ile

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<210> 35

<211> 307

<212> PRT

<213> Synechocystis sp

<400> 35

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Lys Leu Trp Leu Ala Ala Ile Lys Pro Pro Met Tyr Thr Val Ala Val
20 25 30
Val Pro Ile Thr Val Gly Ser Ala Val Ala Tyr Gly Leu Thr Gly Gln
35 40 45
Trp His Gly Asp Val Phe Thr Ile Phe Leu Leu Ser Ala Ile Ala Ile
50 55 60
Ile Ala Trp Ile Asn Leu Ser Asn Asp Val Phe Asp Ser Asp Thr Gly
65 70 75 80
Ile Asp Val Arg Lys Ala His Ser Val Val Asn Leu Thr Gly Asn Arg
85 90 95
30 Asn Leu Val Phe Leu Ile Ser Asn Phe Phe Leu Leu Ala Gly Val Leu
100 105 110
Gly Leu Met Ser Met Ser Trp Arg Ala Gln Asp Trp Thr Val Leu Glu
115 120 125
Leu Ile Gly Val Ala Ile Phe Leu Gly Tyr Thr Tyr Gln Gly Pro Pro
130 135 140
35 Phe Arg Leu Gly Tyr Leu Gly Leu Gly Glu Leu Ile Cys Leu Ile Thr
145 150 155 160
Phe Gly Pro Leu Ala Ile Ala Ala Ala Tyr Tyr Ser Gln Ser Gln Ser
165 170 175
40 Phe Ser Trp Asn Leu Leu Thr Pro Ser Val Phe Val Gly Ile Ser Thr
180 185 190

Ala Ile Ile Leu Phe Cys Ser His Phe His Gln Val Glu Asp Asp Leu
195 200 205
Ala Ala Gly Lys Lys Ser Pro Ile Val Arg Leu Gly Thr Lys Leu Gly
210 215 220
5 Ser Gln Val Leu Thr Leu Ser Val Val Ser Leu Tyr Leu Ile Thr Ala
225 230 235 240
Ile Gly Val Leu Cys His Gln Ala Pro Trp Gln Thr Leu Leu Ile Ile
245 250 255
Ala Ser Leu Pro Trp Ala Val Gln Leu Ile Arg His Val Gly Gln Tyr
10 260 265 270
His Asp Gln Pro Glu Gln Val Ser Asn Cys Lys Phe Ile Ala Val Asn
275 280 285
Leu His Phe Phe Ser Gly Met Leu Met Ala Ala Gly Tyr Gly Trp Ala
290 295 300

15 Gly Leu Gly
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<210> 36

<211> 927

<212> DNA

<213> Synechocystis sp

<400> 36

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cctgcttccc	tggatttagt	gttcggcgct	tggctggcct	gcctgttggg	taatgtgtac	180
attgtcggcc	tcaaccaatt	gtgggatgtg	gacattgacc	gcatcaataa	gccgaatttg	240
cccctagcta	acggagattt	ttctatcgcc	cagggccggt	ggattgtggg	actttgtggc	300
gttgcttcct	tggcgatcgc	ctggggatta	gggctatggc	tggggctaac	ggtgggcatt	360
agtttgatta	ttggcacggc	ctattcgggt	ccgccagtga	ggttaaagcg	cttttccctg	420
ctggcggccc	tgtgtattct	gacgggtcgg	ggaattgtgg	ttaacttggg	cttattttta	480
tttttttaga	ttggtttagg	ttatcccccc	actttaataa	cccccatctg	ggttttgact	540
ttatttatct	tagttttcac	cgtggcgatc	gccattttta	aagatgtgcc	agatatggaa	600
ggcgatcggc	aatttaagat	tcaaacttta	actttgcaaa	tcggcaaaca	aaacgttttt	660
cggggaacct	taattttact	cactggttgt	tatttagcca	tggcaatctg	gggcttatgg	720
gcggctatgc	ctttaaatac	tgttttcttg	attgtttccc	atttgtgctt	attagcctta	780
ctctggtggc	ggagtcgaga	tgtacactta	gaaagcaaaa	ccgaaattgc	tagtttttat	840
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<210> 37

<211> 308
<212> PRT
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Ile Gly Thr Thr Leu Ser Val Trp Ala Val Tyr Leu Leu Thr Ile Leu
20 25 30
10 Gly Asp Gly Asn Ser Val Asn Ser Pro Ala Ser Leu Asp Leu Val Phe
35 40 45
Gly Ala Trp Leu Ala Cys Leu Leu Gly Asn Val Tyr Ile Val Gly Leu
50 55 60
Asn Gln Leu Trp Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asn Leu
65 70 75 80
Pro Leu Ala Asn Gly Asp Phe Ser Ile Ala Gln Gly Arg Trp Ile Val
85 90 95
Gly Leu Cys Gly Val Ala Ser Leu Ala Ile Ala Trp Gly Leu Gly Leu
100 105 110
20 Trp Leu Gly Leu Thr Val Gly Ile Ser Leu Ile Ile Gly Thr Ala Tyr
115 120 125
Ser Val Pro Pro Val Arg Leu Lys Arg Phe Ser Leu Leu Ala Ala Leu
130 135 140
Cys Ile Leu Thr Val Arg Gly Ile Val Val Asn Leu Gly Leu Phe Leu
145 150 155 160
25 Phe Phe Arg Ile Gly Leu Gly Tyr Pro Pro Thr Leu Ile Thr Pro Ile
165 170 175
Trp Val Leu Thr Leu Phe Ile Leu Val Phe Thr Val Ala Ile Ala Ile
180 185 190
30 Phe Lys Asp Val Pro Asp Met Glu Gly Asp Arg Gln Phe Lys Ile Gln
195 200 205
Thr Leu Thr Leu Gln Ile Gly Lys Gln Asn Val Phe Arg Gly Thr Leu
210 215 220
Ile Leu Leu Thr Gly Cys Tyr Leu Ala Met Ala Ile Trp Gly Leu Trp
225 230 235 240
35 Ala Ala Met Pro Leu Asn Thr Ala Phe Leu Ile Val Ser His Leu Cys
245 250 255
Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser
260 265 270
40 Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe
275 280 285

Leu Glu Tyr Leu Leu Tyr Pro Leu Ala Leu Trp Leu Pro Asn Phe Ser
290 295 300

Asn Thr Ile Phe
305

5

<210> 38
<211> 1092
<212> DNA
<213> Synechocystis sp

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<400> 38
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gaaaatcctg ctagcgatca tcattacggc ggcggtgctg tgcaaatttt agggccggct 180
acgaaaaaac aagaaaatca ggaagaccaa cttgtttggc ggacatttcc ctcggtaaaa 240
aaattttggg ccagtcctcg ccagtttgcc ctagggcatt ggggaaaatg tagggataac 300
aggcaggcga aaccctact ctccgaagaa ttttttgcca cggtaagga aggttatcaa 360
atccatcaaa atcagcacca aggacaaatc attcatggcg atcgccattg tcgttggcag 420
ttcaccgtag aaccggaagt aacttggggg agtcctaacc gatttcctcg ggctacagcg 480
ggttggcttt cttttttacc cttgtttgat ccggttggtc aaattctttt agccaagggt 540
agagcgcacg gctggctgaa atggcagagg gaacagtatg aatttgacca cgccctagtt 600
tatgccgaaa aaaattgggg tcaactcctt cctcccgct ggttttggt ccaagcaaat 660
tattttcctg accatccagg actgagcgtc actgccgctg gcggggaacg gattgttctt 720
ggtcgccccg aagaggtagc ttaattggc ttacatcacc aaggtaattt ttacgaattt 780
ggccccggcc atggcacagt cacttggaac gtagctccct ggggccgttg gcaattaaaa 840
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<210> 39
<211> 363
<212> PRT

35 <213> Synechocystis sp

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20 25 30

Ser Phe Ala Phe Met Tyr Ser Ile Glu Asn Pro Ala Ser Asp His His
 35 40 45
 Tyr Gly Gly Gly Ala Val Gln Ile Leu Gly Pro Ala Thr Lys Lys Gln
 50 55 60
 5 Glu Asn Gln Glu Asp Gln Leu Val Trp Arg Thr Phe Pro Ser Val Lys
 65 70 75 80
 Lys Phe Trp Ala Ser Pro Arg Gln Phe Ala Leu Gly His Trp Gly Lys
 85 90 95
 Cys Arg Asp Asn Arg Gln Ala Lys Pro Leu Leu Ser Glu Glu Phe Phe
 10 100 105 110
 Ala Thr Val Lys Glu Gly Tyr Gln Ile His Gln Asn Gln His Gln Gly
 115 120 125
 Gln Ile Ile His Gly Asp Arg His Cys Arg Trp Gln Phe Thr Val Glu
 130 135 140
 15 Pro Glu Val Thr Trp Gly Ser Pro Asn Arg Phe Pro Arg Ala Thr Ala
 145 150 155 160
 Gly Trp Leu Ser Phe Leu Pro Leu Phe Asp Pro Gly Trp Gln Ile Leu
 165 170 175
 Leu Ala Gln Gly Arg Ala His Gly Trp Leu Lys Trp Gln Arg Glu Gln
 180 185 190
 20 Tyr Glu Phe Asp His Ala Leu Val Tyr Ala Glu Lys Asn Trp Gly His
 195 200 205
 Ser Phe Pro Ser Arg Trp Phe Trp Leu Gln Ala Asn Tyr Phe Pro Asp
 210 215 220
 25 His Pro Gly Leu Ser Val Thr Ala Ala Gly Gly Glu Arg Ile Val Leu
 225 230 235 240
 Gly Arg Pro Glu Glu Val Ala Leu Ile Gly Leu His His Gln Gly Asn
 245 250 255
 Phe Tyr Glu Phe Gly Pro Gly His Gly Thr Val Thr Trp Gln Val Ala
 260 265 270
 30 Pro Trp Gly Arg Trp Gln Leu Lys Ala Ser Asn Asp Arg Tyr Trp Val
 275 280 285
 Lys Leu Ser Gly Lys Thr Asp Lys Lys Gly Ser Leu Val His Thr Pro
 290 295 300
 35 Thr Ala Gln Gly Leu Gln Leu Asn Cys Arg Asp Thr Thr Arg Gly Tyr
 305 310 315 320
 Leu Tyr Leu Gln Leu Gly Ser Val Gly His Gly Leu Ile Val Gln Gly
 325 330 335
 Glu Thr Asp Thr Ala Gly Leu Glu Val Gly Gly Asp Trp Gly Leu Thr
 340 345 350
 40 Glu Glu Asn Leu Ser Lys Lys Thr Val Pro Phe

355

360

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<211> 56

5 <212> DNA

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<211> 32

<212> DNA

<213> Artifical Sequence

<400> 41

tcgaggatcc gcggccgcaa gcttcctgca gg

32

<210> 42

<211> 32

<212> DNA

<213> Artifical Sequence

<400> 42

tcgacctgca ggaagcttgc ggccgcggat cc

32

<210> 43

<211> 32

<212> DNA

<213> Artifical Sequence

<400> 43

tcgacctgca ggaagcttgc ggccgcggat cc

32

<210> 44

<211> 32

<212> DNA

<213> Artifical Sequence

<400> 44

tcgaggatcc gcggccgcaa gcttcctgca gg

32

<210> 45

<211> 36

<212> DNA

5 <213> Artificial Sequence

<400> 45

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36

10 <210> 46

<211> 28

<212> DNA

<213> Artificial Sequence

15 <400> 46

cctgcaggaa gottgcggcc gcggatcc

28

<210> 47

<211> 36

<212> DNA

<213> Artificial Sequence

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tcgacctgca ggaagcttgc ggccgcggat ccagct

36

<210> 48

<211> 28

<212> DNA

<213> Artificial Sequence

30

<400> 48

ggatccgcgg ccgcaagctt cctgcagg

28

<210> 49

35 <211> 39

<212> DNA

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<400> 49

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<210> 50
<211> 31
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<213> Artifical Sequence

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<400> 50
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<210> 51

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<211> 41
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<400> 51
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<210> 52

<211> 38

<212> DNA

<213> Artifical Sequence

<400> 52
ggatcctgca ggtcacttca aaaaaggtaa cagcaagt 38

<210> 53

<211> 45

<212> DNA

<213> Artifical Sequence

30 <400> 53
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<211> 40

35

<212> DNA
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<210> 55

<211> 38
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5 <400> 55 38
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<210> 56
<211> 37

10 <212> DNA
<213> Artifical Sequence

<400> 56 37
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15 <210> 57
20 <211> 50
25 <212> DNA
30 <213> Artifical Sequence

<400> 57 50
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35 <210> 58
40 <211> 38
45 <212> DNA
50 <213> Artifical Sequence

30 <400> 58 38
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<210> 59
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<212> DNA
35 <213> Artifical Sequence

<400> 59 38
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40 <210> 60
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<212> DNA

<213> Artifical Sequence

<400> 60

36

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<210> 61

<211> 22

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10 <213> Artifical Sequence

<400> 61

22

taatgtgtac attgtcggcc tc

5 <210> 62

<211> 60

<212> DNA

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60

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<210> 63

<211> 22

<212> DNA

<213> Artifical Sequence

<400> 63

22

aggctaataa gcacaaatgg ga

<210> 64

<211> 63

<212> DNA

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<400> 64

60

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63

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<211> 26

<212> DNA

<213> Artifical Sequence

<400> 65

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5 ggatccatgg ttgcccaaac cccatc

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10 <213> Artifical Sequence

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61

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<212> DNA

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ccc

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<210> 69

<211> 23

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<213> Artifical Sequence

<400> 69

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ccagtggttt aggctgtgtg gtc

40

<210> 70

<211> 21
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5 <400> 70
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<210> 71

<211> 28

10 <212> DNA
<213> Artifical Sequence

<400> 71
ggatccatgg ttacttcgac aaaaatcc 28

<210> 72

<211> 60

<212> DNA

<213> Artifical Sequence

<400> 72
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<211> 28

<212> DNA

<213> Artifical Sequence

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<210> 74

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35 <213> Artifical Sequence

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40 <210> 75

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<211> 22

10' <212> DNA
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<400> 76 22
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15' <210> 77

<211> 28

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<213> Artifical Sequence

20' <400> 77 28
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25' <210> 78

<211> 62

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<210> 79

<211> 27

35 <212> DNA
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<400> 79 27
gaattctcaa atccccgcat ggcctag

40 <210> 80

<211> 65
<212> DNA
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5 <400> 80
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gtggg 65

<210> 81
10 <211> 21
<212> DNA
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15 <400> 81
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<210> 82
<211> 21
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20 <213> Artifical Sequence

<400> 82
gcaatacccg cttggaaaac g 21

25 <210> 83
<211> 29
<212> DNA
<213> Artifical Sequence

30 <400> 83
ggatccatga ccgaatcttc gcccctagc 29

<210> 84
<211> 61
35 <212> DNA
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<400> 84
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40 g 61

<210> 85
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<210> 86
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<210> 88
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<210> 89
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<400> 89
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<210> 90

<211> 0

<213> Artifical Sequence

5 <400> 90

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<211> 4550

10 <212> DNA

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cgattaagat taggaaaaat ttataaccgg taattaagaa aacattaacc gtagtaaccg	180
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taacattagc tctgtgattg gatttgcagg tgcttagcat tttatctgta tctttcttag	1620
cagtagagaa ggtttctgat atatctcctt tacttttcac tggcatcttg gaggtaatga	1680

5
 10
 15
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 35
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<212> DNA

<213> Arabidopsis sp

<400> 92

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10 <211> 2850

<212> DNA

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<400> 93

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<211>

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35 <213> soy

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<212> PRT

5 <213> soy

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15 <211>

<212> PRT

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45 AAAACGACCTTGTGTTTACACTACCAAGGGAGGTTAACTCTAGTTTTTATGTGACCACTT
ACCTTGAGAGTTGAGACCATGGAATCACTTGTGCACTCCTCGGCTTGTATATTCTAGTG
TCAGCATTTGCATTTCTCTCCCACTTGTACTTGAAAAGTTGAAGACAACCTTTTTTGTGTT
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<210> 100

50 <211>

<212> DNA

<213> wheat

55 CGTCCGCGGACGCGTGGGTGCTTATTCAGTCAATCTGCCGCACTTCTATGGAAGAGATC
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TTTTCTCCACATTGACATTTGTTTTTCAGAAGGCCGGCAGACTTTTCAAAGCCATTGAT
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CGATATTGAAGGGGACCGCATCTTTGGAATCCAATCTTTTAGTGGTAGACTAGGTCAAAG
CAGGGGTTTCTGGACTTGGCTTGGCTACTTGGGTTGCCTACGGTGTGCGATACTGAG
5 GGGGGTAACCTCTTCCAGTTTGTGGAGCAAATCTATAACTGTTGTGGGCCATGCAATCCT
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<210> 101

10 <211>

<212> DNA

<213> leek

15 GTTTCCCCCCTCGAATTTTTTTTTTTTTTTTTTACTTCATTTTTCTGTGAATAAATTCT
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TGATAATCTTTAACACAACATACAACATGAATATAATTAAGGAGAAATGATCTGCAATTG
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20 TCTTACAAAAGGAATGAGCAAGTACTCAGCATAGAAGAGCTTCCACACGAACATATAAAA
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CCCAAGAATTGCATGACCTATCACTGTTAAGCATTGCTCCATAGGCATGAGGAAGTAGC
TCCAACAACCATGACAACAGTGTAGGCCATCTCAAGGAGATATATACATATCCAAAACAC
CCTCTCCTGGCCAAGGCGCACGCTGAAAGAATGGATGCCAAATATTTTGTCTCCGCTCAT
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5 AAATATCAATGGCCTTGTGAAACTTGCTGGTCTTTTGAACAAA

<210> 102

<211>

<212> DNA

30 <213> leek

15 NATTCGGCACGAGTTTGAAGAAGTTAAGCATGGACTCCCTCCTTACCAAGCCAGTTGTA
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CATGTGAAACCAAGGTTTACAACATGTAGTAGGTCTCAAAAACCTGGTCATGTAAAAGCC
ACATCCGAGCATCTTTAGAATCTGGATCCGAAGGATACACTCCTAGAAGCATATGGGAA
GCCGTACTAGCTTCACTGAATGTTCTATACAAAATTTTCACGACCTCACACAATAATAGGA
ACAGCAATGGGCATAATGTCAGTTTCTTTGCTTGTGTGCGAGAGCCTATCCGATATTTCT
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40 ATTGTAGGTCTGAATCAATTATTTGACATAGAAATAGACAAGGTCAATAAACCTGATCTT
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<210> 103

45 <211>

<212> DNA

<213> canola

50 TTTTTTTTTTTTTTTTTTCAAAAAGACCAATCCTTTAGTATGTACAT
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ATTCCATATAAACCGGTAATATCCTGCTATAGCTTCCCTTGTGTAGTTTGGCTTTTCTAG
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ACCTCTAAAAACCTGAGGCATGTAGAAAGCTAGTGATATGGCAGAAATATAGTTCAGTAG
55 CAGAAGTCCAGAACCGAGGAATGCAATGTTCTCACTCCAAGCTTGTGTAGTGTGA
TATTTGGAAGTTGCGATCTCCTTCAACATCAGGAAGATCTTTGTAAATAGCAATGACTAG
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TCCAAGAGCAGCTCTAGTAGCATGGTACACACCAAAATTAAGAAGAAAACCTCGTACCGT
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5 <210> 104
<211>
<212> DNA
<213> corn

10 CCACGCGTCCGCCCCGCCAAGGGATGGACGCGCTTCGCCTACGGCCGTCCCTCCTCCCCG
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GAAATGGTGAAGGACGAATTTGCTTTTCTAGCCAAAGGACCCAAGGTCTACCTTGATC
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ATACCTCTGTTAATGCTTCGGGGCAACAGCTGCAGTCTGAACCTGAAACACATGATTCTA
15 CAACCATCTGGAGGGCAATATCATCTCTCTAGATGCATTTTACAGATTTTCCCGGCCAC
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TGTCTGATATATCACCTTTGTTCCCTCACTGGTTTGCTGGAGGCAGTGGTAGCTGCCCTTT
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20 TTTCCGCTCTTTGCCGCTATGAGCTTTGGCCTTGATGGGCTGTTGGATCACAACTCTGT
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5 TATTCAAGGATATACCTGACATCGAAGGGGACCGCATATTCCGGATCCGATCCTTCAGCG
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GCAAAGCCGCAATAACGTCCTTCTACATGTTTCTGGAAGCTGTCTACGCGGAGTACC
10 TGCTCATCCCTCTGGTGCGGTGAGCGCGAGGCGAGGTGGTGGCAGACGGATCGGCGTCCG
CGGGGCGGCAAACTCCACGGGAGAACTTGAGTGCCGGAAGTAAACTCCCGTTTGAAA
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5 <210> 105
<211>
<212> DNA
<213> corn

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CCGTGCGGCCCGCGCGGCCCGCGAGATCATTTTCTACCACCATGTTGTTCCATAC
45 AACGAAATGGTGAAGGACGAATTTGCTTTTCTAGCCAAAGGACCCAAGGTCTACCTTGC
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TAAATACTTCTGTTAATGCTTCGGGGCAACAGCTGCAGTCTGAACCTGAAACACATGATT
CTACAACCATCTGGAGGGCAATATCATCTTCTCTAGATGCATTTTACAGATTTTCCCGGC
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50 TTTTCATGAATATCTATATTGTTGGACTGAACAGTTATTTCGACATTGAGATAGACAAGG
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55 TGATTGTTGAGCTGGCCTTTTCTCCACATTGAGCTTTTGTGTTTTCAGGAGACCGGAG
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60 TCGCTGGCCATTCCATACTTGCCGCGATCCTATGGAGCTGCGCGGATCGGTGGACTTGA
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CAGTGACCCAACTTGGTGGGCTGAGCTCAGCGCTCAGCAGCTTTACGTGCATCTGCGCC
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<210> 106

<211>

<212> DNA

<213> corn

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CCCTCCACTCCACTTGCTCACTCGTGGCTCGTCCGCGCCCGCTTCCCCCGGCAAGG
GATGGACGCGCTTCGCTACGGCCGTCCTCCTCCCGTGCGGCCCGCGCGCCCGCCCG
GCGAGGCGAGTGGTAGCTGCCCTTTTCATGAATATCTATATTGTTGGACTGAACAGTTAT
TCGACATTGAGATAGACAAGGTTAACAAGCCAACCTTCCATTGGCATCTGGGGAATACA
CCCTTGCAACTGGGTTGCAATAGTTTTCGGTCTTTGCCGCTATGAGCTTTGGCCTTGGAT
GGGCTGTTGGATCACAACCTCTGTTTTGGGCTCTTTTCATAAGCTTTGTTCTTGGGACTG
CATATTCAATCAATCTGCCGTACCTTCGATGGAAGAGATTGCTGTTGTTGAGCACTGT
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<210> 107

<211>

<212> DNA

<213> cotton

CCCACGCGTCCGAACATTGTTTGCACTTGTTATTGCCATAACCAAGGATCTTCCAGATGT
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TGCAATTTCTTGGTTCCGGACTTCTACTGGTGAATTATGTTGCTGCTGTTGGCTGCAAT
ATACATGCCTCAGGCTTTTCAAGCGTAGTTTAAATGATACCTGCTCATATCTTTTGGCGGT
CTGCTTGATTTTTAGACATGGGTGTTGGAACAAGCAAATTACAAAAGGAAGCAATCTC
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<210> 108

<211>

<212> DNA

<213> tomato

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GTTGCAGCGGCAGTATATCACGCAAGAGCATGTTGGAGGAAGTGATCTAAGCACTATTGC
TGCTGATAAAAACTTAAAGGGAGATTTTGGTGCACGCATCATCTGAACACCTCTTGA
ATCTCAACCTTCTAAAGTCCCTGGGACTCAGTTAATGATGCCGTAGATGCTTTCTACAG
GTTCTCGCGGCCCATACCATATAGGAACAGCATTGAGCATAATTTAGTTTCTCTCCT
TGCAGTTGAGAAGTTCTCTGATTTTCTCCATTATTTTCACTGGGGTGTAGAGGCCAT
TGTGCTGCCCTATTTCATGAACATTTACATAGTTGGTTTAAACAGTTGTCTGACATCGA
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<210> 109

<211>

<212> DNA

<213> *Arabidopsis*

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TGTATCTCCTCTCACTCGCTCACTAGTTCGGTTCGATCGACTAACTAGTTCCCCGCTC
CATTCTAGGGGGATCCCGTCGATCTCCACCCCGAATAGTGAACTGACAAGATCTCCGT
TAAACCTGTTTACGTCCCGACGTCTCCCAATCGCGAAGTCCGGACTCCTCACAGTGGATA
10 CCATTTTCGATGGAACACCTCGGAAGTCTTCGAGGGATGGTGGATCCGGGTTTCCATCCC
AGAGAAGAGGGAGAGTTTTTGTGTTTATGTATTCTGTGGAGAATCCTGCATTTCCGCAGAG
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TCTTGGCGCTAATGATAAATATTTATGCCAATACGAACAAGACTCTCACAAATTTCTGGGG
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15 AAACAAGGAGGTTCCACCAGAGGAATTTAACAGAAGAGTGTCCGAAGGGTTCCAAGCTAC
TCCATTTTGGCATCAAGGTCACATTTGCGATGATGGCCGTACTGACTATGCGGAACTGT
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CAAACAGAAGTCAACTGCAGGCTGGCCTGCAGCTTTTCCTGTATTTGAGCCTCATTTGGCA
GATATGCATGGCAGGAGGCCTTTCCACAGGGTGGATAGAATGGGGCGGTGAAAGGTTTGA
20 GTTTCGGGATGCACCTTCTTATTCAGAGAAGAATTGGGGTGGAGGCTTCCCAAGAAAATG
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25 AGAGGCAAGAACAAATGAAGCGGGTACACCTCTGCGTGCTCCTACCACAGAAGTTGGGCT
AGCTACGGCTTGCAGAGATAGTTGTTACGGTGAATTGAAGTGCAGATATGGGAACGGCT
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30 CTTCAAGCCACCGGGTCTGTAACATTGATGAGTGTTTTGTTGTTGATAGAGACCATGT
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<210> 110

35 <211>

<212> PRT

<213> *Arabidopsis*

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IPEKRESFCFMYSVENPAFRQSLSPLEVALYGPRTGVGAQILGANDKYL
CQYEQDSHNFWDGRHELVLGNTFSAVPGAKAPNKEVPPEEFNRRVSEGFQ
ATPFWHQGHICDDGRDYAETVKSARWEYSTRPVYWGWDVGAQKQSTAGW
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45 KWFVWQCNVFEGATGEVALTAGGGLRQLPGLTETYENAAALVCVHYDGMY
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GLATACRDSCYGELKLQIWERLYDGSKGVILETKSSMAAVEIGGGPWFG
TWKGDTSNTPPELLKQALQVPLDLESALGLVPFFKPPGL*